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Page 1

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GenCore version 5.1.5
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	May 25, 2003, 13:21:49 ; Search time 1037 Seconds (without alignments) 5107.725 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-762-105A-14 183-99-762-105A-14 1 9agotogetceccogcogtctgactggtggacaggctagc 182
Scoring table:	IDENTIFY_NUC Gapop 10.0 , Gapext 1.0

4109280 Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2054640 seqs, 14551402878 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

in\_fun: in. GenEmb1:\* Database :

em\_htg\_inv:\* em\_htg\_other:\* em\_sy:\* em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htg\_vrt:\* em\_sts: am\_pat : VO\_IIIS

am\_or:

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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## ALIGNMENTS

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AF176637 5270 bp DNA linear SYN 24-APR Plastid transformation vector pWSK49 plastid targeting region. AF176637.1 G1:7637848	Plastid transformation vector pWSK49. Plastid transformation vector pWSK49 artificial sequences; vectors. The pass 1 to 5270; Khan, S. and Maliga,P. Pluorescent artibiotic resistance marker for tracking plastid transformation in higher plants. Nat. Biotechnol. 17 (9), 910-915 (1999)
RESULT 1 AF176537/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	SCURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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AX137514 127 bp
Sequence 16 from Patent EP1076095.
AX137514
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complement(3881, ..3885)

//ncte="errill/7gl0+nb/Rc promoter and translation control region contained in Sac1-Nhel fragment."

//ncte="sac1, Ecost and sat1 restriction sites"

//ncte="sac1, Ecost and sat1 restriction sites"
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374 ATTTGTTAACTTTAAGAGAGAATATACATATGGCAAGCATGACGAGGGGGGAGGACAGGCTA 5685
                                                                                                                                                                                                                                                                                                                                                                 3804 AGGGGCAGGGAFGGCTATATTCTGGGAGGGAGCCACAACGGTTCCCACTAGAATA 3745
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                                                                                                                                                                                                                Gaps
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                                                                                                                                                                   Length 5270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified.
(Lebses 1 to 168)
Staub, J.W.
Enhanced expression of proteins using gfp
patent: Wo 0104331-A 1 18-JAN-2001;
Calgene LLC (US)
                                                                                                                                                                   Query Match
100 0%; Score 182; DB 12;
Best Local Similarity 100.0%; Pred: No. 1e-47;
Matches 182; Conservative 0; Mismatches 7;
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Sequence 1 from Patent WO0104331.
AX076661.1 GI:12711193
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/db_xref="taxon:32644"
31 c 51 g 41
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PAT 31-JAN-2002
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Nakashita. Wamaguchi, I., Yoshioka, K. and Doi, Y. Process for producing polyester
Process for producing polyester
Patent: UP 2001046074.A 16 20-FEB-2001;
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Toddoh, N. Shinozaki, K. and Sugiura, M.
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PN 10-201046074-A/16
PN 10-201046074-A/16
PN 10-201046074-A/16
PN 10-201046074-A/16
PN 10-201046074-A/16
PN 10-201046074-A/16
PN 10-20104074-A/16
PN 10-201
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         64
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                                             11 TIGCTCCCCCCCCCCCTCCATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGG
    5 TCGCTCCCCCCCCCTCGTTCAATGAATGGATAAGAGGCTCGTGGGGATTGACGTGAGGG
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Pred. No. 7.8e-17;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                       DNA
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/organism="Nicotiana tabacum"
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E51197
                                                                                                                                                                         11 GGCAGGGATGCTATATTTCTGGGAGCGA 99
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24 c 45 q
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Best Local Similarity 97.8%;
Matches 87; Conservative
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Nicotiana tabacum.
Nicotiana tabacum
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VERSION
KEYWORDS
SOURCE
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TITLE
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KEYWORDS
SOURCE
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                                                                                           Nicotiana tabacum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Solanates; Solanaceae; Nicotiana...
I (bases I to 127)
Yamaguchi... Nakshita.H., voshitoka.K. and Doi, Y.
Panaguchi... Nakshita.H., voshitoka.K. and Doi, Y.
Potene: Ep 1076095-A 16 14-FEB-2001;
Patene: Ep 1076095-A 16 14-FEB-2001;
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Nakabilta, Nicotiana, Nicotiana
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Pred. No. 7.8e-17;
0; Mismatches 2;
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    127
    /organism-"Nicotiana tabacum"

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/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
1 24 c 45 g 30 t
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    AX137514.1 GI:14273708
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JP 2001046073-A/16.
Nicotiana tabacum.
Nicotiana tabacum
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1 Similarity 97.8%;
87; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 c
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                                                                         common tobacco
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CHNPTRNVI Thear PAR 04-UNI-1993 A part of the Chicar Park 04-UNI-1993 A pumbaginicity and tring genes for 165 ribosomal RNA, transfer RNA'v1 and transfer RNA-ILE (5'exon).
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Errbosomal RNA: Inverted repeat; ribosomal RNA; transfer RNA;
transfer RNA-IIe-qua; transfer RNA-Val-qac; trni qene; trny gene.
Chiloroplast Nicotiana plumbaginifolla
Bakaryota; Viridiplantese streptophyta; mbryophyta; racheophyta;
Spermatophyta; Magnollophyta; endicotyledons; core endicota;
Spermatophyta; Magnollophyta; endicotyledons; core endicota;
Spermatophyta; Magnollophyta; endicotyledons; core endicota;
(bases 2059 to 2418)
Challic, Horvath, C., Nervath, E., Dix.P.7; and Medgyesy, P.
Chloroplast transformation in plants; polyethylese glycol (PEG)
treatment of protoplasts is an alternative to biolistic delivery
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   Query Match 47.1%; Score 85.8; DB 8; Length 2113; Bast Local Similarity 97.8%; Pred. No. 14-16; 2; Indels 0; Matches 87; Conservative 0; Mismatches 97; Conservative
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/dev_stage="mature plant"
/gene_trnv*
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/note-"5'exon"
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Horvath, G.V.
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Tobacco Totorplast genes for 16s Tibosomal RNA and tRNA-Val.
NOMIGE JOL453
WO0165.1 GI:11799
WO0165.1 GI:11799
WO0165.1 GI:11799
S. 16s Tibosomal RNA: Tibosomal RNA: transfer RNA: transfer RNA-Val.
Common tobacco.
ISM Minhammal RNA: Tibosomal RNA: Tibosomal RNA: transfer RNA-Val.
Schemetophyta: Wagnolophyta: General Rna-Valle
RNA: Tibosomal 
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                                                                                                                           tRNA sequence contributed on tape April 1983 by M.Sprinzi 6 transs; from their entry 2063 in Nucleic Acids Res. 11, r55-r103 (1983). [1] proposes bases 302 or 308 as possible sites for transcription initiation, based on an in vitro assay with E.coli
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/product="tRNA-Val"
//note="codon recognized: GUC; Val-tRNA (NAR: 2063)"
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Sequence of a putative promoter region for the rRNA genes tobacco chloroplast DNA mucleic Acids Res. 9 (20), 5399-5406 (1981) 7029469
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WLLAASRKRPGRNMAFKLSSELVDAAKGSGDAIRKKEETHRMAEANRAFAHFR"
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initiation factor; inverted repeat, maturasa; MADH dehydrogenase;
PSI 9RD protein, PSI I-protein, PSI J-protein, PSI 9P700 apoprotein,
PSII 10kD phosphoprotein; PSII 32kD protein; PSII 4kD protein;
PSII 4XD protein; PSII cytochrome b559; PSII D2 protein; PSII
I-protein; PSII J-protein; PSII K-protein; PSII L-protein; PSII
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Pred. No. 1.2e-16;
0; Mismatches 2;
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/protein_id="CAB41472
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'codon_start=1
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/gene="ndhB"
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165 Tibosomal RNA: 165 TRNA gene; NADH dehydrogenase subunit; ndhB
gene; ribosomal protein 512; ribosomal protein 57; rps12 gene; rps7
gene; transfer RNA-Ala; transfer RNA-ILB; transfer RNA-Val;
tRNA-Ala gene; tRNA-Ile gene; tRNA-Val gene.
                                                                                                                                                                                                                                                                                                                                                                                      /uly pp DNA linear PLN 29-MAR-2001
Solamn igrum chloroplast tRNA-lla, tRNA-lla, 16S TRNA, tRNA-Val,
19512, rps7, ndh8 qenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lack nightshade.
Plastid Solanum nigrum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnollophyta; eudicotyledons; core eudicot; Asteridae; eusscerids; Solanacee; Solanum.
14 (bases 1 to 7829)
15 (bases 1 to 7829)
16 (bases 1 to 782)
17 (bases 1 to 782)
18 (bases 1 to 782)
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                                                                                                           TCGCTCCCCCCCCCTCGTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGG 64
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Submitted (19-APR-1999) T.A. Kavanagh, University of Dublin,
Department of Genetics, Trinity College, Dublin 2, IRELAND
Location/Qualifiers
1. 7829
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Pred. No. 1.1e-16;
0; Mismatches 2; Indels
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join <5498. :5729,6266. :6291)
/gene="rps12"
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/gene="rps12"
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/product="16S ribosomal RNA"
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/organelle="plastid"
                                                                                                                                                                                                                          1088 GCCAGGGATGCCTATATTTCTGGGAGCGA 1116
                                                                                                                                                                                                65 GGCAGGGATGGCTATATTTCTGGGAGGGA 93
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3797, 3860
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/gene="tRNA-val"
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/gene="tRNA-Ile"
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circular PLN 27-JUL-2001

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I (bases I to 15544).

Shinozaki, K., Ohme, M., Tanaka, M., Wakasuqi, T., Hayashida, N., Marabayashi, T., Zaita, N., Chunvongest, J., Obofala, J., Mangotchi-Shinozaki, K., Ohto, C., Torazawa, K., Meng, B. Y., Sugita, M., Peno, H., Kanogashira, T., Yamada, K., Meng, B. Y., Sugita, M., Pohdoh, N., Shimada, H. and Sugiura, M. The complete nucleotide sequence of tobacco chloroplast genome:its
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Nadot, S., Elttar, G., Carter, L., Lacrolx, R. and Lejeune, B.
A phylogenetic analysis of monocotychedous based on the chloroplast
gene rps4, using parsimony and a new numerical phenetics method
Mol. Phylogenet. Evol. 4 (3), 257-282 (1995)
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Fine mapping of replication origins (ori A and ori B) in Nicotiana
tabacum chioroptast DNA
     Laja: ribosomal protein Lajz: ribosomal protein Lajs: ribosomal protein Lajs: ribosomal protein Sil; ribosomal Sil; ribosoma
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Submitted (27-FEB-1998) T. Tsudzuki, Data Processing Center,
Aichi-Gakuin University, 12 Aralke, Twasaki, Nisshin, Aichi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \label{eq:michelson,K.} \begin{tabular}{ll} 
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Morton, B. R. and Clegg, M.T.
Mortonollast DNA mutational hotspot and gene conversion noncoding region near rbcL in the grass family (Poaceae) 54077 395 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the sequenced chloroplast genomes
Nucleic Acids Res. 19 (5), 983-995 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene organization and expression
EMBO J. 5, 2043-2049 (1986)
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Pred. No. 1.6e-16;
0; Mismatches 2;
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ABE315582 156697 bp DNA CITCULAR PLN 05-APR-2002 ALTO ALTODA belladonna Complete Plastid Chromosome, strain Abbp(kan).
AJ315582 ALTOSOMAL STADOSOMAL RNA, 4.55 ribosomal RNA, 58 ribosomal RNA, 238 ribosomal RNA, 4.55 ribosomal RNA, 58 ribosomal RNA, 50 ribosomal RN
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ABE316582
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                                                                                                                                                                                                       This designated zero and numbered proceeding towards LSC. The DNA strand which codes for the large subunit of Fublose complementary strand as B strand send strand as B strand send self-strand self-s
on or before Jan 17, 2002 this sequence version replaced gi:264799, gi:11807.
                                                                                                         for election tobacco chloroplast DNA sequence is presented in a inearized form by cutting at the junction (JLA) between IRA and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-protein; rbci_gene: rtbosomal_protein_Lid; 
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                                                                                                                                                                                                                                 Submitted (24-MAY-2000) Schmitz-Linneweber C., Botanisches Institut, Ludwig Maximilians Universitaet Muenchen, Menzinger Str. 67, Muenchen, Bavaria 80638, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                     proof gene, pash gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The nucleotide sequence of the plastid chromosome of Atropa beladona (deadly nightshade) and its comparison with that of Nicotiana tabacum with emphasis on sequence elements relevant for
S subunit; ndhA gene; ndhB gene; ndhC gene; ndhD ndhF gene; ndhG gene; ndhH gene; ndh gene; ndh KH 489; petA gene; petB gene; petD gene; petG petN gene; petG petN gene; potGetN gene; potential heme-binding protein; PSI
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protein; ycf4 gene; ycf2 gene; Ycf2 protein; ycf3 gene; YcF3
bclladonna.
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tRNA-Ser(UGA) gene; tRNA-Thr (GGU) gene; tRNA-Thr(UGU) gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tRNA-Tyr(GUA) gene; tRNA-Val (GAC)
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Herrmann, R.G. and Maier, R.M
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                                                                    Schmitz-Linneweber, C.
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          dehydrogenase ND5
                                                                         ndhE gene; ndhK gene; petL gene; p
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                                                                                                                                                                                                                                                 gene;
P700
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SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL FEATURES

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/translation="MPTINQLIRNTRQPIRNVTKSPALRGCPQRRGTCTRVYTITPKK
PNSALRKVARVRLTSGFEITAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGTL
                                                                                                                                                                                                                                                                                                                                                                  complement(100360. .100894), complement(100333. .100359),
complement(74748. .72591),142431. .142662,143198. .143223)
/genea-ment(74748. .72591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÝSYFI I ÁT LÁ ÞPYD I DGI REPVSGSLLYGNNI I SGALI PPSAALGLHFP PIRBAASY
DEMI NGGPYELI VILHET LIGNGYNGREMELSFRLÓMRPHI INVETI
TOGGSS SOGAP LÁ LSGTR NPH I PROMEHI LIMHP PHILOFYGSLESARHSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AWPVVGIWFTALGISTMAFNLNGFNFNQSVVDSQGRVINTWADIINRANLGMEVMHER
NAHNPPLDLAAIEAPSTNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation-"MEEIQRYLQPDSSQQHNFLYPLIFQEYIYALAHDHGLNINRSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVY ECESTFVFLRNOSSHLRPTSFGALLERIYFYGK I ERLVEVFAKDLQVTLMLFKDP
FMHYVRYQGKSILASKGTFILLINKWKFYLVNFWQCHFSLCFHTGRIHINOLSNHSRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNSALRKVARVRLTSGFEITAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTAILERRESESLWGRFCNWITSTENRLYIGWFGVLMIPTLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTSSLIRETTENESANEGYRFGQEEETYNIVAAHGYFGRLIFQYASFNNSRSLHFFLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEI PFSLRLISSLSSFEGKKILKSHNLRSIHSTFPFLEDNFSHLNYVLDILIPYPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEILVQTLRYWVKDASSLHLLRFFLHEYWNLNSLITSKKPGYSFSKKNKRFFFLYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPTINQLIRNTRQPIRNVTKSPALRGCPQRRGTCTRVYTITPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .100359,100895. .101126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          oin(complement(72478, .72591),142431, .142662,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //gene="tRNA-Lys (UUU)"
/product="text"
                                                                                                                                                                               /product-"ribosomal protein S12"
/protein_id-"CAC88091.1"
/db_xref-"G1;20068378"
                                                                                                                                                                                                                                                                                                                                                    .101126),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"ribosomal protein S12"
/protein_id-"CAC88068.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="PSII 32 kD protein"
/protein_id="CAC88024.1"
/db_xref="GI:20068311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"codon recognized: AAA"
complement(1769. .1804)
l. .156687
/organism="Atropa belladonna"
/strain="Ab5p(kan)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"codon recognized: CAC"
complement(494. .1555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAC88025.1"
/db_xref="G1:20068312"
                                                                                               complement(join(100334.72478. .72591))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2068. .3597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4323)
                                                                                                                                                                                                                                                                                                                                                |oin(complement(100895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5, .82)
/gene="tRNA-His (GUG)"
/product="tRNA-His"
                                                                         /db_xref-"taxon:33113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"GI:20068355"
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/gene="psbA"
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                                                                                                                                                                                                                                                                                                                          DAVGVKDROQGRSKYGVKKPK
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complement(2068, .359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .143223)
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                                                                                                                                                         /codon_start=1
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/gene="rps12"
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us-09-762-105a-14.rge

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gene; pett gene; petw gene; potential heme-binding protein; PSI prog approrectin AI, pash gene; pas
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Segmatophyta; Magnollophyta; eudicotiedons; Oarc eudicots;
Agteridae; cussterids I; Solanaies; Solanaces; Atropa.
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1. 156687
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Herrmann,R.G. and Maler,R.M.
The nucleotide sequence of the plastid chromosome of Atropa
belladonna (deadly nightshade) and its comparison with that of
Nicotiana tabbcum with emphasis on sequence elements relevant for
microcyclution
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/strain="Ab5p(kan)"
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2 (bases 1 to 156687)
Schmitz-Linneweber, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Atropa belladonna
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                                                                                                                                                                                                                                                                                                                                                                                           /unimet=1 (5050. .6138)
/gene=rpsiG
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                                                    MOTISSVALNPSWVRSQMLENSFIINMIKKFPULVPIPLIGISKAKRYGYTHRY
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                                                                                                                                                                                        complement (4324 . 4360)
/gene="tknk-Lys (UUU)"
/product="tknk-Lys"
/note="complement (4324 . 4580)
/number=1
/number=1
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// Gene Press (699. 6138)
// Gene Press (699. 6138)
// Gene Fress (786. 7431)
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// Gene Fress (786. 7431)
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// Fress (786. 7431)
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/gene="rps16"
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/product="thosomal protein S16"
/Protein_id="thosomal protein S16"
/Dr. xef='01:20068313"
/Tansitalo='MYRIXERGERYBRAVRIVAIDVRSREGKDLRKVGFVDPIKN
OFFLINPALLYFLERGAGPGFVGDTLKKARVFRELREPROFRFI"
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Bogoslan,G., O'Nell,J.P. and Staub,J.M.
Bacterial expression systems based on plastic or mitochondrial
promoter combinations
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/gene="rps16"
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1.6e-16;
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Pred. No. 1.1e-16;
0; Mismatches 1;
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Location/Qualifiers
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                                                                                       /note="codon recognized:
complement(4324. .4360)
                                                                                                                                                                                                                                                                                                                                                                                               complement(5050, .5276)
/gene="rps16"
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complement(7360. .7431
/gene="tRNA-Gln (UUG)"
                                           /gene="tRNA-Lys (UUU)"
/product="tRNA-Lys"
                                                                                                                             /gene="tRNA-Lys (UUU)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"tRNA-Gln"
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/number=1
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97.88;
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                                                                                  /product-Tribosomal protein S12.
/product-Tribosomal protein S12.
/protein_id-"cAc88091.1"
/protein_id-"Ac88091.1"
/cranslation-"MPTINQLIRNTRQPIRNVTKSPALRGCPQRRGTCTRVTITPRK
/cranslation-"MPTINQLIRNTRQPIRNVTKSPALRGCPQRRGTCTRVTITPRK
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SROWSDLENSOSI LDBREGKCHALFHYS SUSSKRKTAFRIKTIL STROKARKIKS
TYRTEKRSGSBLLEBFLISEDOVLSLTFPRASSSIMGTY RSTRYLDIFOTHDLAN
                                                                                                                                                                         PNSALRKVARVRLTSGFEITAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGTL
                                                                                                                                                                                                                  join(complement(100895, .101136),
complement(100360, .1010894), complement(100333, .100359),
complement(7240786, .75591), 442431, .142662, 143198, .143223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MPTINQLIRNTRQPIRNVTKSPALRGCPQRRGTCTRVYTITPRKR
PNSALRKVARVRLTSGFEITAYIPGIGHNLQEHSVVLVRGGRVKDLPGVRYHIVRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MTAILERRESESIMGRFCNWITSTENRLYIGWFGVLMIPTLLTA
ISVFIIAFIAAPPVDIDGIREPVSGSLLYGNNIISGAIIPTSAAIGLHFYPIWEAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YP IGGGESDGAPLAISCTERFMYPGAEHNIAMPEHMIGYAGYGGGSLFSAMHGSL
VYSSLIRETTERSANEGY REGGESETVYVAÄNGIYGERILFOVAR STRUKSELHEPLA
AMVYOTETTÄLISTÄMÄRUMGERFOUSVUSGGRY INTMADIIRAKUGHEKVHERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     procein 1d-"cac88055.1"
/db_xref-"ci 2006831-2007
/transiation-"mercrippdssoohnelypliforytvalahdhglninrsil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEILVQTLRYWVKDASSLHLLRFFLHEYWNLNSLITSKRPGYSFSKKNKRFFFFLYNS
YVYECESTFVFLRNQSSHLRPTSFGALLERIYFYGKIERLYEVFAKDLQYTLMLFKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEWLYNGGPYELIVLHFLLGVACYMGREWELSFRLGMRPWIAVAYSAPVAAATAVFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENPGYNNQFSLLIVKRLITRMYQQNHFLISTNDSNKNTFLGCNKSLYSQMISEGFAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEIPFSLRLISSLSSFEGKKILKSHNLRSIHSTFPFLEDNFSHLNYVLDILIPYPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMHYVRYQGKSILASKGTFLLINKWKFYLVNFWQCHFSLCFHTGRIHINQLSNHSRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1769. .1804,1805. .4323,4324. .4360))
gage="tenkhrips (UU)"
complement(join(1769. .1804,4324. .4360))
/gane="tenkhrips (UUU)"
                    complement(join(100334. .100359,100895. .101126,
                                                                                                                                                                                                                                                                                                       join(complement(72478. .72591),142431. .14262,143198. .143223)
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/gene**tRNA His (GUG)*
complement(5. 82)
/gene**tRNA His (GUG)*
/product="tRNA-His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="tRNA-Lys (UUU)"
complement(2068. .3597)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2068. .3597)
/db_xref-"taxon:33113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAVGVKDRQQGRSKYGVKKPK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(494. ,1555)
                                                                                                                                                                                                    DAVGVKDRQQGRSKYGVKKPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAHNFPLDLAAIEAPSTNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"maturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product-"tRNA-Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1805.
                                           (2478. .72591))
                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                   codon_start.
                                                                                                                                                                                                                                                                                      'gene-"rps12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "dene-"psbA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene-"matK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"matK"
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**LRNA** gene

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gene

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0;

2 GCTCCCCCCCCCCTCGTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 61

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| December | December
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Search completed: May 25, 2003, 14:05:05 Job time : 1177 secs

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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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May 25, 2003, 13:38:09 ; Search time 61 Seconds (Without alignments) 915.003 Willion cell updates/sec
OM nucleic - nucleic search, using sw model
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                                                    Run on:
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1 gagetegeteeceegeegte......tgactggtggacaggetage 182

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Sequence:

Total number of hits satisfying chosen parameters: 441362 segs, 153338381 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued\_Patents\_NA:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2\_6/ptodata/z/ina/3b\_COMB.seq:\*
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		ď			SUMMARIES		
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-	9.68	49.2	171	7	US-08-217-360-16	Sequence 16, Appl	
7	86.4	47.5	129	~	US-08-189-256A-25	Sequence 25, Appl	
m	86.4	47.5	129	4	US-09-193-853-25	25,	
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'n	98	47.3	140	4	US-09-193-853-19	19,	
9	98	47.3	164	7	US-08-189-256A-26	26,	
7	86	47.3	164	4	US-09-193-853-26		
œ	85.4	46.9	161	N	US-08-189-256A-18	18,	
6	85.4	46.9	161	4	US-09-193-853-18	18,	
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11	85.4	46.9	165	4	US-09-193-853-4	4	
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13	85.4	46.9	168	4	US-09-193-853-2	7	
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18	85.4	46.9	300	4	US-09-202-316-7	7	
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50	85.4	46.9	1134	4	US-09-193-853-10	Sequence 10, Appl	
21	85.4	46.9	1143	4	US-09-142-114B-6	6, A	
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56	85.4	46.9	1417	4	US-09-142-114B-7	7, 4	
27	85.4	46.9	2962	~	US-08-189-256A-3	'n	

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Gaps

22;

Length 171; Indels

DB 1;

1.4e-21

Score 89.6; DI Pred. No. 1.4e 0; Mismatches

Query Match Best Local Similarity 78.3%; Matches 130; Conservative

GCTCCCCCCCCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66

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Appl
                                                                             App1
                        Sequence 7
Sequence 7
Sequence 7
Sequence 7
Sequence 1
Sequence 1
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Sequence 3
Sequence 1
                                                                                     Sequence Sequence Sequence
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                                                                                                                        Sequence
              US-09-597-877-9
US-08-06-182A-7
US-08-877-109-7
US-08-799-766-7
US-08-217-360-13
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US-09-337-028-9
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US-08-929-967-1
US-08-929-967-3
US-08-929-967-3
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METHODS FOR PRODUCING CYTOPLASMIC
MALE STERLLITY IN PLANTS AND USE THEREOF IN PRODUCTION OF H
MARIE STERLITY AND USE THEREOF IN PRODUCTION OF H
                                                                                                                                                                                                                         ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSEE: P.C.
ADBRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Vorsion #1.25
CURREWF PRDICATION DAMA:
PRILICATION NUMBER: US/08/217,360
CLASSIFICATION: 800
CLASSIFICATION: 800
MANE: REED, Janet B.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: Rutgers University TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                 Sequence 16, Application US/08217360 Patent No. 5530191 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (215)563-4100
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215)563-4044
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 171 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       Philadelphia
                                                                                        APPLICANT: MALIGA,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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US-08-217-360-16
                                                                                                                                                                                                                                                                                                                 STATE:
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CCGCCGTCT TTGGCTATAT TTGGCTATAT TGGCTATAT SP11cat10 8168	Zora Zora A. Jeffrey A. Jeffrey A. Joil A. T. Helain B. N. Incastorming Plastid N. Expessing Penatid N. Expessing Penatid N. Expessing Penatid N. Expessing Penatid N. Expessing Penatid N. Expessing Penatid DESS: 47 DESS: 48 DESS: 4	Query Match  Guery Match  Best Local Similarity 89:4%; Fred. No. 15-20; Length  Matches 99; Conservative 0; Mismatches 11; Indels 0; Gaps  Matches 99; Conservative 0; Mismatches 11; Indels 0;  A COTCOCCOCCOCCOTORITY MANAGEMENT AND
	THE STANDARD ZZZDB OD W. STEELSEWED SAMEN AND CO. CREWEN	TOPOLOGY: linear

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TITLE OF INVENTION: DNA Constructs and Methods for Stably TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Expressing Recombinant Proteins Therein WOHERS OF SEQUENCES: 47 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 GCTCCCCCCCCCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGGATTGACGTGAGGGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 GCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGACGCTCGTGGGGATTGACGTGAGGGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Leus. 2.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 CAGGGATGGCTATATTTCTGGGAGGGAGCCACACACGGTTTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 CAGGGATGGCTATATTTCTGGGAGCGAACTCCGGGCGAATTC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                        :: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 86; DB Pred. No. 2.1e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/193,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-189-256A-26
Sequence 26, Application US/08189256A
; Patent No. 5877402
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,256
                                                        Svab, Zora
Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
Kanevski, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (215) 563-4100
(215) 563-4044
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.28
Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                       Maliga, Pal
                                                                                                                                                                                                                                                                                                                                  CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                19103-2307
                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-09-193-853-19
                                    APPLICANT:
                                                        APPLICANT:
APPLICANT:
                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         STATE:
Patent No.
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                                                                                                                                                                                                                                                                                     TITLE OF INVERTION: TANA CONSTRUCTS and Methods for Stably
TITLE OF INVERTION: Transforming Plastids of Walticellular Plants and
TITLE OF INVERTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 GCTCCCCCCCCCCTCCTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGCGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 GCTCCCCCCCCCCCTCCTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.3%; Score 86; DB 2; Length 140; 90.2%; Pred. No. 2.1e-20; tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 CAGGGATGGCTATATTTCTGGGAGGGAGACCACAACGGTTTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMAE: PactorIn Release #1.0, Version #1.30
SOFWMEE: PactorIn Nomber: APPLICATION NAMER: US/08/189,256A
RFILING DATE: 31-JAN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Warket Street Suite 720
CITY: Pilladelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/518,763 FILING DATE: 01-MAY-1990 ATTORNEY/AGENT INFORMATION:
                                                                      Sequence 19, Application US/08189256A
Patent No. 5877401:
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
                                                                                                                                                                                   Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                    Kanevski, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                             Svab, Zora
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Best Local Similarity
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US-08-189-256A-19
                                 RESULT 4
US-08-189-256A-19
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Svab, Zora Staub, Jeffrey

APPLICANT: APPLICANT:

Sequence 19, Application US/09193853

RESULT 5 US-09-193-853-19

APPLICANT: Maliga, Pal

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Sequence 18 Application US/08189256A
Sequence 18 Application US/08189256A
Sequence 18 Application
Sequence 18 Application
Sequence 18 Application
APPLICANT: Stabb Jeffrey
APPLICANT: Stabb Jeffrey
APPLICANT: Allabarko, Oleg V.
APPLICANT: Allabarko, Lori A.
APPLICANT: Remerkel, Ivan
APPLICANT: Remerkel, I
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Expressing Recombinant Proteins Therein UNDER OF SEQUENCES: 47 CORRESSONDENCE ADDRESS: ADDRESSE: 10 CORRESSONDENCE ADDRESS: 10 CORRESPET: 10.0 Market Street. Sulte 720 STREET: 10.0 Market Street. Sulte 720 CTRIT. Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2302
ZUP: 19103-2302
COMPUTER READALE FORM:
MEDIUM TYPE: FIDEPP disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
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CLASSITICATION:
PRIOR APPLICATION: DAYA:
PRIOR APPLICATION NAMER:
PRIOR APPLICATION NAMER:
PRIOR APPLICATION NAMERA:
PRIOR APPLICATION NAMERAY-1907
APPLING DAYE:
RECORD RESEARCH OF THE STATEMENT (215) 563-4100
THE LEDSTHEE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
EDSTHEE CHARACTERISTICS:
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TERSTHEE CHARACTERISTICS
THE CHARACTERIST
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US-09-193-853-26
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                                                                                                                                               APPLICANT: Allied V.
APPLICANT: Remeable V.
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Transforming Plastids of Multicellular Plants V.
TITLE OF INVENTION: Expressing Recombinant Proteins Therein COMPRESS: Allied V.
ADDRESSE: Allied V. APPLICANTON: Expressing Recombinant Proteins Therein COMPRESS: Allied V.
STATE: PA.
COUNTRE: PA.
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Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
Kanevski, Ivan
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APPLICANT: Carrer,
APPLICANT: Kanevski
TITLE OF INVENTION:
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HYPOTHETICAL: N
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US-08-189-256A-26
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TITLE OF INVENTION: DNA CONSTRUCTS and Methods for Stably TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and TITLE OF INVENTION: Expressing Recombinant Proteins Therein
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MEDIUM TYPE: Floppy disk
CMBOTTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pettentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
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Pred. No. 3.6e-20;
0; Mismatches 1;
                                                                                                                                                                                                                                                                          APPLICATION WIMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: REGG/ Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/193,853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/08189256A
; Patent No. 5877402
                                                                                                                                                                                                                    APPLICATION NUMBER: 08/189,256
                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4010
TELEPA: (215) 563-4044
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zoubenko, Oleg V. APPLICANT: Allison, Lori A. APPLICANT: Carrer, Helaine
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  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 98.98
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
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Svab, Zora
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ADDRESSEE: Dann, Dor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                      FILING DATE:
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US-09-193-853-18
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                                                                                                                            E: Floppy disk
IMB PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
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STREET: 1601 Market Street Suite 720
  Suite 720
                                                                                                                                                                                                                                                                                             PRIOR MURLICATION DATA:
APPLICATION NUMBER: US 06/111,398
FILING DATE: 2-AUG-1993
PRIOR APPLICATION DATA: US 07/518,763
FILING DATE: US 07/518,763
APPLICATION NUMBER: US 07/518,763
APPLICATION NUMBER: US 07/518,763
APPLICA
                                                                                                                                                                                                        CURRENT APPLICATION DARS

APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
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Patent No. 6388168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMUNICATION INFORMATION:
TELEPHONE: (215) 563-4004
INFORMATION FOR SEC ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 161 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Svab, Zora
Staub, Jeffrey
Zoubenko, Oleg V.
Allson, Lori A.
Carrer, Helaine
Kanevski, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
1601 Market Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 98.9
Matches 86; Conservative
                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                      Philadelphia
                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                              COUNTRY: USA
ZIP: 19103-2307
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APPLICANT:
APPLICANT:
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APPLICANT:
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ZIP: 191
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APPLICANT: Walls of the Management of Manag
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CONTRY: TIGSA
CONTRY: TIGSA
CONTRY: READABLE FORM:
MEDIUM TIFE: FORDY
MEDIUM TIFE: FORDY
MEDIUM TIES: TIBN FC. CONTRY:
OPERATING STSTAR: PC-DOS/MS-DOS
CONTRARE: Petentin Release: 11.0, Version #1.30
CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/09/193,853
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46.94, Score 85.4; DB 2; Best Local Similarity 98.94; Prod. No. 3.7e-20;
Matches 86; Conservative 0; Mismatches 1;
CURRENT APPLICATION DATA:
APPLICATION WHORE: US/08/189,256A
FLING DATE: 31-3AN-1994
CLASSIFCATION: 455
PRIOSE STECATION WHORE: 455
PRIOSE APPLICATION WHORE: 465
PRIOR APPLICATION WHORE: 467
APPLICATION WHORE: 467
PRIOR APPLICATION WHORE: 467
FLING DATE: 25 AUG-1993
PATOR APPLICATION WHORE: 467,222
PRECESTATION WHORE: 467,222
TELECOMONICATION INFORMATION:
TELEPAK: (215) 563-4104
TRELEPAK: (215) 563-4104
TRELEPAK: (215) 563-4104
TRELEPAK: (215) 563-4104
TRELEPAK: (215) 563-4104
TYPE: AUGUSTICE CHARACTERISTICS:
LENGHY: 165 Date parts
TYPE: AUGUSTICE CHARACTERISTICS:
LENGHY: 165 Date parts
TYPE: AUGUSTICE: 110001
STREAM CONTACT STREAM
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PRIOR APPLICATION DATA:
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APPLICANT: Stabb. Policy
APPLICANT: Stabb. Policy V.
APPLICANT: Stabb. Policy V.
APPLICANT: Allison. Lori A.
APPLICANT: Allison. Lori A.
APPLICANT: Allison. Lori A.
APPLICANT: Armsevski, Ivan
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF EXQUENCES: A7
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, DOFTMEN, HOTTELL and Skillman
STREET Dann, DOFTMEN, HOTTELL and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 46.94; Score 65.4; DB 47. Length 165; Best Local Smalarity 98.94; Pred No. 3.7e-20; Messer Local Smalarity 98.94; Pred No. 3.7e-20; Messer Messer 86; Conservative 0; Hismatches 16; Conservative 0; Hismatches
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                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLING DATE:
ATTORNEY CARRY THORNAY TON:
NAME: Reed, James: 36, 22
TELECOMONICATION NUMBER:
TELECOMONICATION S. 65-4410
TELECOMONICATION S. 65-4410
TELECOM
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CAUTER READABLE FORM: IN FROMPOTER READABLE FORM: IN FROMPOTER PROPERATION OF STREET IN FOR COMPACTION OF STREET FC. TOOK 785. PLOS
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APPLICATION NUMBER: 08/189,256
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Svab, Zora
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ANTI-SENSE: NO
US-09-193-853-4
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ORGANISM: Nicotiana tabacum.
  (215) 563-4044
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                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                       : 168 base pairs
nucleic acid
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                                                                                                                                                                                                                                                      86; Conservative
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Matches 86; Conserv
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                                                                                       STRANDEDNESS:
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APPLICANT:
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  TELEFAX:
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                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                      Score 85.4; DB 2; Length 168;
Pred. No. 3.7e-20;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
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FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Read Jamet E.
REGISTRATION WUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/193,853
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                                                TELECOMAUTICATION INCORATION:
TELECOMAUTICATION INCORATION:
TELEFAX (215) 563-4100
INCORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERSTICS:
INRGTH: 108 Date pales
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-193-853-2
; Sequence 2, Application US/09193853
; Patent No. 6388168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2IP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                               REGISTRATION NUMBER: 36,252
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TELEPHONE: (215) 563-4100
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Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
Carrer, Helaine
                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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Best Local Similarity 98.9%;
Matches 86; Conservative
ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: not relevant
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APPLICANT: Svab, Zora
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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US-08-189-256A-2
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APPLICANT:
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APPLICANT BOGOSLIA, Gregg
APPLICANT: O'NEIL, Julia P.
APPLICANT: Stanb, Jeffrey
TITLE OF INVENTION: Mitochondrial Expression Systems Based on Plastid or
TITLE OF INVENTION: Mitochondrial Promoter Combinations
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                                                                                                                                                    Score 85.4; DB 4;
Pred. No. 3.7e-20;
0; Mismatches 1;
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Pred. No. 3.8e-20;
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CURRENT FILING DATE: 1999-04-01
BARLIER APPLICATION NUMBER: 60/080,432
RARLIER FILING DATE: 1998-04-02
SARLIER FILING DATE: 1998-04-02
SOFWARE: PATENTING OFFE: 38
SOFWARE: PATENTIN VET: 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                               61 CAGGATGCCTATATTTCTGGGAGCGA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09283419A Patent No. 6218145
STRANDEDNESS: single TOPOLOGY: not relevant . MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                       46.9%;
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98.9%;
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Staub, Jeffrey
Zoubenko, Oleg V.
Allison, Lori A.
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us-09-762-105a-14.rni

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DNA Constructs and Methods for Stably
Transforming Plastids of Multicellular Plants and
Expressing Recombinant Proteins Therein
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RELIANG DATE: 31-34N-1999
RELIANG DATE: 32-34NG-1993
RELIANG DATE: 105-34NG-1993
RELIANG DATE: 105-34NG-1993
RELEPRANCE TO NOT NATION NUMBER: 35,22
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REL
TITLE OF INVERTION: DNA CONSTRUCES and Methods for
TITLE OF INVERTION: Transforming Plastids of Muli
TITLE OF INVERTION: Expressing Recombinant Prote-
NUMBER OF SEQUENCES: 47
CORRESPONDRICE ADDRESS:
ONDESSEE: Denn. Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
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ZIP: 19103-2307
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TOPOLOGY: 11n
MOLECULE TYPE:
HYPOTHETICAL: N
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US-08-189-256A-24
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17 GCTCCCCCCCCTCCTTCAATGAGAATGGATAAGAGGCTCGTCGGGTTGACGTGAGGGGG 76 7 GCTCCCCCCCCCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG 66 Query Match 46.9%; Score 85.4; DB 2; Length 258; Best Local Stanlarity 98.9%; Pered. No. 4.4e-20. Makiches 86; Conservative 0; Mismatches 1; Indels Matches 86; Conservative 0; Mismatches 1; Indels ò

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Search completed: May 25, 2003, 14:27:51 Job time : 62 secs

77 CAGGGATGGCTATATTTCTGGGAGCGA 103

us-09-762-105a-14.rnpb

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Sequence 13, Appl
Sequence 1, Appli
Sequence 4, Appli
                                                                                        May 25, 2003, 13:41:49; Search time 104 Seconds (Without alignments) 2310.809 Million cell updates/sec
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Sequence 1, ?
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"Gqn2_6/prodata/2/pubma/U806_URW_UB.seq:"
"Gqn2_6/prodata/2/pubma/U806_PUBCOMB.seq:"
"Gqn2_6/prodata/2/pubma/U806_PUBCOMB.seq:"
"Gqn2_6/prodata/2/pubma/U806_PUBCOMB.seq:"
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-088-475-12
US-09-813-718-9
US-09-917-107-49
US-09-967-107-49
US-09-967-107-45
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US-09-987-107-63
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: COTORILIO, SYLVIC
APPLICANT: LUID, METTY SYLVIC
TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the
TITLE OF INVENTION: Plastids of Higher Plants
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                                                                                                                                                             Sequence 5, A
Sequence 7, A
Sequence 1, A
Sequence 11, A
Sequence 5, A
Sequence 5, A
Sequence 15, Sequence 15, Sequence 15, Sequence 13, Sequence 17, A
Sequence 13, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 17, Sequence 26, Sequence 
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Pred. No. 3.4e-21;
0; Mismatches 39;
08.09.987.107.43

08.09.987.107.43

08.09.987.107.45

08.09.987.107.67

08.09.987.107.67

08.09.987.107.67

08.09.813.718.3

08.09.813.718.1

08.09.97.297.7

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US-09-981-002-5
US-10-212-357-1
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SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030088081A1
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Best Local Similarity 75.0%;
Matches 117; Conservative (
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; ORGANISM: tol
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                                                1 GAGCTCGCTCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 113, Application US/0940925A
Publication to US2000054338A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GIVEN MARK AND D.
GIVEN DAVID M.
TITLE OF INVENTION: BAPED DEFECTION AND IDENTIFICATION OF
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NUMBER OF SEQUENCES. 165

CORRESPONDENCE ADDRESS. CARROLL

STREET STREET, SUITE 2200

STREET STREET STREET, SUITE 2200

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STREET CALIFORNIA

COMPUTER RANACHE FORM:

REDIGINATIVE FLORPY disk

COMPUTER RANACHE FORM:

REDIGINATIVE FLORPY DISK

COMPUTER TRANCHE FORM:

REDIGINATIVE FACTOR COMPATION:

REDIGINATION HUMBER: 10, Version #1.30

CURRENT APPLICATION HUMBER: 24,09

ATTORNEY ADDRESS: 2,433

REDIGINATION HUMBER: PORE OF REDIGINATION HUMBER: PORE OLITICATION HUMBER: PORE OLITI
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                                                                                                                                                                                                                                                                Sequence 1, Application US/09843324A
; Patent No. US20020042934A1
; GENERAL INFORMATION:
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APPLICANT: Ye, Gu
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US-09-843-324A-1
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US-09-940-925A-163
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Sequence 4, Application US/10109612

Sequence 4, Application US/10109612

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Sequence 1. Application US/10109812

Sequence 1. Application Wo. US2030088081A1

SEREMAL INFORMION: US2030088081A1

APPLICANT: WILLY KELY

TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the TITLE OF INVENTION: High Level Expression of Immunogenic Proteins in the TITLE OF INVENTION: Plant 1030 CHIGHER PLANTS

FILE REPEBRACE: RANGEREE: USA/0.109, 812

CURRENT PLICATION WIRESE: USA/0.109, 812

CURRENT PLICATION WIRESE: QC-21.39

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

SOFTWARE: Estado for Windows Version 3.0

SOFTWARE: Estado for Windows Version 3.0

SED ID NO 1

TYPE: DATE

TYPE: DA
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; ORGANISM: tobacco
US-10-109-812-4
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US-10-109-812-4
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US-10-109-812-1
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GENERAL INFORMATION:
APPLICANT: De Francesco, Raffaele
APPLICANT: De Francesco, Raffaele
APPLICANT: TOME, LICIA
APPLICANT: TOME, DER REPRODUCING IN VITRO THE
TITLE OF INVENTION: RNA-DEPENDENT RNA DOINTERASE AND TERRITALA NUCLEOTIDYL
TITLE OF INVENTION: TRANSFRABE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
TITLE OF INVENTION: TRANSFRABE ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILL REPRENCE: TOOOLOCA
CURRENY TALLIA DATE: 2002-02-37
FRIOR PILIA DATE: 2002-02-39
PRIOR PILIA DATE: 1996-03-23
PRIOR APPLICATION NUMBER: 096/592-981
PRIOR PILIA DATE: RM55A000343
PRIOR APPLICATION NUMBER: 1955-05-24
NUMBER: 05 SEQ ID NOS: 14 035-05-25
SUSTRARES OF SEQ ID NOS: 14 040-08 Version 4.0
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                                          APPLICANT: Luiz Kerry 1712.

TILE OF INVENTION: High Level Expression of Immunogenic Proteins in the TILE OF INVENTION: High Level Expression of Immunogenic Proteins in the TILE OF INVENTION: Plastida of Higher Plants

TILE REPRESEME: Rutos=2-00-0038 CIP

CURRENT FILE DATE: 2000-00-29

PRIOR PAPLICATION NUMBER: PC7/US00/25930

PRIOR PAPLICATION NUMBER: 60/211,139

PRIOR FILING DATE: 2000-06-13

PRIOR FILING DATE: 1999-06-21

PRIOR FILING DATE: 1999-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 GAGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 GAGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTATAAGAAGGAGATA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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68.9%; Pred. No. 3.1e-13;
Live 20; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 41
LENGTH: 89
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100.0%; Pred
0; M
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                  Cornellle, Sylvie
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Conservative
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US-10-109-812-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 TACATATGGC 157
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Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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APPLICANT: Stauly Jeffrey
APPLICANT: To, Guangling
APPLICANT: To, Guangling
APPLICANT: Wethod for the transformation of plant cell plastids
TITLE OF INVENTION: Wethod for the transformation of plant cell plastids
CURRENT APPLICATION NUMBER: US/09/643,324A
CURRENT APPLICATION NUMBER: US/09/643,324A
RUGHENT FILEN DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 2
SEQ ID NOS: 2
LENGTH: 244
TITLE OF INVENTION BETOLISS, Debra or the transformation of plant cell plastids PFILE REPRESENTE: 15869/Web Hethod for the transformation of plant cell plastids CHRENT RELIGION WINDER: US/09/4843,324A CHRENT FILING DATE: 2010-04-25 PRIOR PFILING DATE: 2010-04-25 PRIOR PFILING DATE: 2010-04-25 SOFFWARE: PAGE ID NOS: 2 SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 77.8; DB 10; Length 202;
Pred. No. 3e-16;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic construct US-09-843-324A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09843324A Patent No. US20020042934A1 GENERAL INFORMATION:
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Publication No. US203030088081A1
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 TGGCTATATTTCTGGGAGGGA 93
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 97.5%;
Matches 79; Conservative
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US-10-109-812-41

RESULT 7

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Query Match

Matches

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89 AGGGAACCACAACGGIITCCCACIAGAAAIAANITIGIITTAACIITAAGAAGGAGAIAI 148
3364 AGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATAT 3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 36.7%; Score 66.8; DB 9; Length 1057; Best Local Smilarity 97.1%; Fred. No. 36-12; 2; Indels 0; Matches 68; Conservative 0; Mismatches 79; Indels 0.
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Patent No. US2020156007A1

GENERAL INFORMATION

APPLICANT: GENERAL SERVING SEASON

APPLICANT: GENERAL SEASON

APPLICANT: WESTON AND ADDRESS SEASON

APPLICANT: WESTON AND ADDRESS SEASON

CURRENT PETING DATE: 2001-01-11-13

PRIOR PETING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: US 60/264,022

PRIOR APPLICATION NUMBER: US 60/264,022

PRIOR APPLICATION NUMBER: DOB-01-15

PRIOR APPLICATION NUMBER: DOB-01-15

PRIOR APPLICATION NUMBER: DOB-01-15

PRIOR APPLICATION NUMBER: DOB-01-15

WHING PATENT NOM PRIOR : 2001-01-15

WHING PATENT SEASON NOM SERVING SEASON NOM SEASON NOM SERVING SEASON NOM SEA
                                                                                                                                                                                                                          OTHER INFORMATION: pt7 H6 Fx Cys-Apo Al plasmid NAME/KRY: CDS LCANTON: (100)...(882) OTHER INFORMATION: US-20-987-107-51
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                                                                149 ACATATGGCAAGCA 162
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US-09-987-107-49
                                                                                                                                                                                                  RESULT 11
US-09-987-107-51
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OSCIPLIANT: PAPLICATION US/09813718

DABLICARTION NO. USZOOD182666A1

CREMERAL INFORMATION: Paul

APPLICART: SCHIMME, Paul

APPLICART: SCHIMME, Paul

APPLICART: WARKSHION: The Regulation of Anglogenesis

TITLE OF INVERTION: The Regulation of Anglogenesis

FILE REPRENENCE: 00-0248ER: US/09/813,718

CURRENT PILING DARE: 2001-03-21

NOTHER OF THE PARENENCE: 2001-03-21

NOTHER OF THE PARENENCE: 2001-03-21
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                                                                                                                                                                                                              NAME/RET. CDS
LOCATION: (3429). (4879)
OTHEN INFORMATION: Description of Artificial Sequence: human
OTHEN INFORMATION: full-length TrpRS in per20B
05-09-813-718-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.8%; Score 68.8; DB 9; Length 9; Best Local Similarity 97.7%; Predi No. 7.2e-13; Indels Margins 70; Conservative 0; Minmiches 2; Indels
                                                                                                                                     Sequence 17, Application US/09897776A Publication No. US20030092001A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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89 AGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATAT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGAGAGATAT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: pT7H6 Trip-A-Apo Al K9A K15A - AmpR plasmid NAME/KEI: COTO.: (100)...(1047)...
OCHER INFORMATION: COTO.: (107)...
OGNER INFORMATION: (107)...
OGNER INFORMATION:
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Pred. No. 3.2e-12;
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3,2e-12;
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Pred. No. 3.2e-
0; Mismatches
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APPLICANT GENERAL JONES
APPLICANT GENERAL SOREN
TITLE OF INVESTRON SOREN
FILE REPERENCE: GRAVERSENIA
PRIOR APPLICATION NUMBER: 08 60/264,022
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2000-10-15
PRIOR PILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 53
FENCE.
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CURRENT FILTME DATE: 2001-11-3
CURRENT FILTME DATE: 2001-11-3
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR PILLE DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR APPLICATION NUMBER: DK PA2000 01682
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; Patent No. US20020156007A1
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97.1%;
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illarity 97.1%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 55
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ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 ACATATGGGA 105
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Matches 68; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                      Length 1088;
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                                                          OTHER INFORMATION: PT7H6 Trip-A-Apo A-1-del 43 - AmpR plasmid WAMF/KB: 100.5 (100) . (1018) . (100) . (1018) . OTHER INFORMATION: 100.5 . (1019) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . (1018) . 
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                                                                                                                                                                                                                                                                  Score 66.8; DB 9;
Pred. No. 3.1e-12;
0; Mismatches 2;
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Pred, No. 3.2e-12;
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APPLICAMY: GENERALY JONAS
APPLICAMY: MOSSYUND, SOZEM
TITLE OF INVENTION: APOLLPOPROTEINS ANALOGUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 47, Application US/09987107
Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/09987107 Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SÖFTWARE: PatentIn version 3.1
SEQ ID NO 47
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QRGANISM: Artificial Sequence
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97.18;
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l Similarity 97.1%;
68; Conservative
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LOCATION: (100)..(1047)
OTHER INFORMATION:
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Matches 68; Conserva
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US-09-987-107-53
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36 AGGAGACCACAACGGTTTCCCTTAGAATAATTTTGTTTAACTTTAAGAAGGAGATT 95

149 ACATATGGCA 158

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APPLICANT: MOESTRUP, SOTEM TITLE OF INVENTION: ADDIDOPROTEINS ANALOGUES FILE REFERENCE: GRAPERSENIA CURRENT APPLICATION NUMBER: US/09/987,107

APPLICANT: GRAVERSEN, Jonas

Query Match

Matches

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us-09-762-105a-14.rnpb

Tue May 27 10:47:40 2003

Search completed: May 25, 2003, 14:29:51 Job time : 107 secs

96 ACATATGGGA 105

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BH558942 BOHL272TR
BH424823 BOHNJ79TR
BH509584 BOHSH07TF
BH472349 BOGIY45TF
BH666002 BOMLN95TF
BH709230 BOMNO33TR
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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd.
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BH653765 BOMNX13TF BH418480 BOGXK95TR	BH474481 BOHHY09TR	BH721450 BOMFR11TR	AQ962940 LERG142TR	BH537952 BOGFU38TR	BH677595 BOMCM49TR	BH474703 BOGQI49TF	BH646726 BOCWR48TF	BH705426 BOMAG13TR	BH430502 BOHJD65TR	BH493122 BOHAC38TF	BH664090 BOMKE52TR	BH662193 BOHWH29TR	BH475597 BOGIS47TF	BH653681 BOHSV92TR	BH545732 BOGKG09TR	BH678091 BOMGJZ0TR		BH689289 BOMLL57TF		BH719545 BOMGP75TF	BH562132 BOGSU17TF	BH541747 BOGFN81TF						341 BOMLI06T		75 BOHTL37T	359	42	995	30	84	BH675079 BOMLS01TF	127
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## ALIGNMENTS

linear GSS 14-DEC-2001	Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Seematophyta; Magnollophyta; endicotyledons; core endicots; Rosidae; eurosids II; Brassicales; Brassicacee; Brassica. I (bases 1 to 787) Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Unpublished (2001) Town, C.D., Town, C.D., Outlease, C.D., Outlease, C.D., Outlease, C.D., Outlease, C.D., Outlease, Delizione, C.D., Outlease, Delizione, C.D., Outlease, C.D., Outlease	
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BH558942 787 bp DNA linear GSS 14-) ABOHL272TR BOHL Brassica oleracea genomic clone BOHL272, DNA AB558942 BH558942. BH558942.1 GI:17810722 BTSSICA oleracea. BTSSICA oleracea.	Dikaryots, Viridiplantes; Streptophyta; Embryophyta; Trach Spermatophyts; Wagnollophyta; eudicotyledons; core eudicot Rosidae; eurosida II; Brassicales; Brassicacee; Brassicales; LOSA) TOWN,C.D., Van Aken,S., Utterback,T. and Fraser,C.W. Whole genome shotgun sequencing of Brassica oleracea Inpublished (2001) Ochec.GSSs: BHLE727F Contact: Chris Town	Table Modified Center Drive, Rockville, MD 20850, USA. Tel: 301-888-3523 Enail: 0208 Enail: cdfown@fig.r.org DNA is from a doubled haploid provided by Tom Osborn. Seq prime: The Second Class: Sheared ends. Location/Qualifiers Location/Qualifiers
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BH558942 BH558942 Sequence HF558942. BH558942.1 GI:17810722 GSS: STRESSICE Oleracea. Brassica oleracea.	Emkarycza, Viridiplani Spermatophyta: Wagoli Rosidae; eurosida II; I (basca I to R87) Town, C. D., Van Aken, S Whole geomome shotgun & Umpublished (2011) Ochez.GSSs: BMLE72FF Contact: Chris Town	9912 Medical Center Drive, R Peal: 301-838 -3023 Fax: 301-838 -002 Fax: 301-838 -002 Fax: 301-839 -002 Seg Primer: The Seg Primer: The Coast: sheared ends Location/Qualifiers
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/clone_lib="BORN"/
/note="Vector: pHGS1; Site_l: BstXI; 2-3 kb sheared
/note="Vector: pHGS1; Site_l: BstXI; 2-3 kb sheared
/note="Vector: pHGS1; Site_l: BstXI linkers"
/note="Vector: phg 164 the pHGS1 using BstXI linkers"
/note="Vector: phg 164 the pHGS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Brassica oleracea"

(db_xref="texon:3712"

(close="Boll:272"

(close="Boll:272"

(note="Vector: pHGSI; Site_1: BstXI; 2-3 kb sheared

(note="Vector: pHGSI; Site_1: BstXI; 2-3 kb sheared

(note="Vector: pHGSI; Site_1: BstXI; 13 kb sheared")

(note="Vector: pHGSI; Site_1: BstXI; 13 kb sheared")

(note="Vector: pHGSI; site_1: BstXI; 13 kb sheared")

(note="Vector: pHGSI; 14 kb sheared")

(note="Vector: phgsI; 15 kb sheared")

(note: phgsI; 15 kb sheared")

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DNA is from a doubled haploid provided by Tom Osboro.
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                      Length 787;
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1911: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                      Score 72.6; DB 17; Length 7 Pred, No. 2.1e-12; 0; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 GGGCAGGGATGGCTATATTTCTGGGAGGGA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 GGGTAGGGTAGCTATATTTCTGGGAGCGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3712"
/clone="BOHNJ79"
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Best Local Similarity 85.3%;
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea.
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BH424823
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ORIGIN
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VERSION
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TITLE
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BH424823
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938 bp DNA linear GSS 13-DBC-2001
BOGIY45TF BOGI Brassica oleracea genomic clone BOGIY45, DNA
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Brassica.
Brassica.
Rosidae.
Brassica.
Brassica.
Brassica.
Brassica.
Town.C.D., Van Aken.S., Utterback.T., and Fraser.C.M.
Whole genome shortgun sequencing of Brassica oleracea
Unpublished (2001)
Conter_GSSS: BG011457R
Contert. Girls Town
H509684 11near GSS 13-DEC-2001
BOHSH077F BOHS Brassica cleracea genomic clone BOHSH07, DNA
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Brassica oleracea.
Brassica oleracea.
Blassica oleracia 
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//db_zrel="taxon:3112"
//clone="bloss="taxon:3112"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA. 191-898-9523 Fax: 301-898-9523 Fax: 301-898-0208 DNA. 15 from a doubled haploid provided by Tom Osborn. Seq primer: TF Class: Theored ends. 17.755 Footballitters
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0; Gaps

GSS 20-FEB-2002

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BH653765 841 bp DNA linear GSS 19-FEB-2002 BOWNX13TF BO_2_3_KB Brassica oleracea genomic clone BOWNX13, DNA
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Spermatophyta; Magnollophyta; eudlocyledonos; one eudlocts;
Rosidae; eurosida; II; Brassicales; Brasslcaceae; Brassica.
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BOWNO33TR BO_2_3_KB Brassica oleracea genomic clone BOWNO33, DNA
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/db_xrei="texon:3712"
/db_xrei="texon:3712"
/clone="Box0033"
/clone_1b="B0.2 3.RB"
/note="Vector: pH0S1; Site_1: BstXI; 2-3 kb sheared
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/note="Vector: pH0S1; Site_2: BstXI inkers"
/note="Vector: pH0S1; Site_2: BstXI inkers"
                                                                                                       4 CTCGCTCCCCCGCCGTCGTTCAATGAGAATGGATAAGAGCTCGTGGGATTGACGTGAGG 63
                                                                          3 GCTCGCTCCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 17; Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rel: 301-638-3523
Fast: 301-898-206
Fast: 101-898-206
Fast: Cctown@tigr.crg
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (base 1 to 0.0 Mills). Brasslcates; Brasslcacee; Bras (base 1 to 0.0 Mills). Utterback, T. and Fraser, C.M. Mole genome shotgun sequencing of Brasslca oleracea Unpublished (2001).
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                12; Indels
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Pred. No. 3.9e-12;
0; Mismatches 47;
            0; Mismatches
                                                                                                                                                                                                 63 GGGCAGGCATGCCTATATTTCTGGGAGGGA 93
                                                                                                                                                                                                                              61 GGGGTAGGGTAGCTATTTCTGGGAGGGA 91
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Best Local Similarity 68.0%;
Matches 100; Conservative (
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                79; Conservative
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Brassica oleracea
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BH653765
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                Matches
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BH709230
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Bukaryota, Viridiantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Brassica.
I (bases I to 770)
Town.C.D., Van Aken.S., Utterbock.T. and Fraser.C.M.
Whole genome shotdun sequencing of Brassica oleracea
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/note="Yector: pHGSI; Site_1: BstXI; 2-3 kb sheared
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/note="Yector pHGSI using BstXI linkers"
a 442 c 191 g 272 t
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Pred. No. 2.9e-12;
0; Mismatches 13; Indels 0,
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TIGR
TYTO Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Tel: 301-838-3528
Email: dotownefigr.org
Email: dotownefigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
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Email: actownetigr.org
New 1s from a doubled haploid provided by Tom Osborn.
Seq primer: PP
Class: Exerced ends.
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/db_xref="taxon:3712"
/clone="BOGIY45"
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86.08;
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Best Local Similarity 86.8%;
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Fax: 301-838-0208
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BH474481 BOHH Brassica oleracea genomic clone BOHHY09, DNA
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/organisms-Brassics oleraces*
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/note="Wector: pH091; Site_1: BstXI; 2-3 kb sheared
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151-881-881-5523
Fax: 301-888-0206
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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/strain-"TO1000H3"
/db_xref-"taxon:3712"
/clone-"BOGXK95"
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Eukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Packaryota, Viridiplantee; Streptophyta; Basicaceae; Brassica.

Fostidae; eurosida II; Brassicales; Brassicaceae; Brassica.

Town, C.D., Van Aken, S., Utterback, T., and Fraser, C.M.

Whole genome shorgum sequencing of Brassica oleracea

Hombilalaed (2011)

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Whole genome Chenton Sequencing of Brassica oleracea Whole genome shotgun sequencing of Brassica oleracea Compublished (2001)
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/clone.lab.ebo.2.ake.li. BetXi; 2-3 kb sheared.
/note.*vector: pHOSI; Site_l: BetXI; 2-3 kb sheared.
/note.*vector: pHOSI; Site_l: BetXI linkers*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9772 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301888-352
874: 101886-352
Email: cdtcomefigr.org
BMA is from a doubled haploid provided by Tom Osborn.
Seq Primer: IF
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1741: 301-838-323
FPA: 301-838-0208
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/organism-*Arabidopsis thallana*
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/fore-*Organ: Leaf: Vector: pUCl9UK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation.*
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Buell, C.R., Lin, X., Pal, G., Barnstead, M., Bowman, C., Utterbach, T., Gelblyum, T., Lidang, F., Creasy, T., and Frasar, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                            Email: atétigr.org
for aditional information, see http://www.tigr.org/tdb/at/at.html
Similar to A. thallana chloroplast sequence (GB:AP000423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dmail: cdrownetigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: Record ends.
Class: Sheared ends.
Location/Qualifiers
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Whole genome shortgus sequencing of Brassica oleracea
Whole genome shortgus sequencing of Brassica oleracea
Other GSSS: BGGFU30FF
Contact: Chris Town
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                                                                                                              polymorphisms
Unpublished (2000)
Contact: Xiaoying in
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Pred. No. 5e-12;
0; Mismatches 12;
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/db_xref="taxon:3712"
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ilarity 86.7%;
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Class: shotgun.
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LERGIATTR LERG Arabidopsis thallana genomic clone LERGIA2, DNA
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Stematophyta; Magnollophyta; endicovjedonas; core endicots;
Rosidae, eurosids II; Brassicales; Brassicaceae; Brassica.
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1 (bases I to 169)
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//db_xref="taxon:3712"
//clone_101b="802_3.xB"
//clone_11b="802_3.xB"
//note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
pendinc Data Inserted faito pHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
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1 (bases 1 to
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/db_xref="texon:3112"
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                                                          /clone_lib="BGGF"
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78: 101-889-828
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BH474703 292 bp DNA linear GSS 13-DEC-2001 BGGQ149TF BOGQ Brassica oleracea genomic clone BOGQ149, DNA
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Spermatophyta, Magnollophyta, eudiocyledons; core eudicots;
Spermatophyta, Magnollophyta, eudiocyledons; core eudicots;
Secides, eucalda II; Brassicales; Brassicaceae; Brassica.
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Whole genome a Lo 305)
Whole genome shotgun sequencing of Brassica cleracea
Unbolished (2001)
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Tel: 301-888-020
Tel: 301-888-020
Email: cdtowneligr.cog
Email: cdtowneligr.cog
Seq primer: Tr
Class: sheared ends.
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// Clone-Brock Trick Tri
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Per Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
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Pred. No. 5.9e-12;
0; Mismatches 12;
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Dmail: cdtownetigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq prime: TF
Class: sheared ends.
1. 305
/ Organism=Brassica oleracea*
/ Streah="Total Composition of the Class of Streah="Total Composition of Stream="Total Composition 
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     OM nucleic - nucleic search, using sw model
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AAZ61386
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AAZ88175
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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# ALIGNMENTS

AA261373 standard; DNA; 182 BP.

RESULT 1

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AAZ61373;

19-JUN-2000 (first entry)

Nucleotide sequence of chimeric promoter PrrnLT7g10+DB/Ec.

Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss Synthetic.

Rey 7.189 (Araq a 7.189 (Araq a 7.189 a 7.189 (Araq a 7.189 a 7.180 a 7.180
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us-09-762-105a-14.rng

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The present sequence represents a DNA construct of the invention. The specification describes recombinant box constructs for expressing heterologous proteins in the plastids of higher plants. The NNA constructs comprise a 5 regular box constructs for expressing the constructs comprise a 5 regular box plants and plants and advanted by the constructs of the heterologous protein methods regular of the heterologous protein methods regular translations estructions of the heterologous protein methods of the plants of the protein protein monocot and diocre plants which leads of the producting production graduation. They can be used the plants of the plants of proteins with agromatic, industrial are poducted like human heemoglobin, industrial or household enzymes which can be transformed with the constructs health, barloy, once, zye or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant DNA constructs, for expressing high levels of heterologous protein in plastical of higher plants, includes promoter, a leader sequence and a downstream box element
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                                                                                                                   /*.tag* b
//noise- aadA sequence*
1035..1755
/*tag* c
//noise- "green fluorescent protein region*
//noise- "green fluorescent protein region*
//noise- "psDA region"
                                                a
"T7 phage gene 10 downstream box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1961 BP; 552 A; 430 C; 486 G; 493 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 100.0%; Score 182; DB 21; Best Local Similarity 100.0%; Fred. No. 2.9e-50; Best Local Similarity 100.0%; Wismatches 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 32; 164pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Khan MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0095163.
98US-0095167.
98US-0112257.
99US-0131611.
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                                                                                                                                                                                                                                                                                                                                          W0200007431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1998;
15-DEC-1998;
29-APR-1999;
11-JUN-1999;
                         misc_feature
                                                                                                misc_feature
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                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a chimeric plastid rRNA operon conserving (Frrin) promoter with the 17 phage gone and plastid conserving (Frrin) promoter with the 17 phage gone and plastid consistent by the constructs for expressing sequence, to produce reconstant to the plastid of higher plants. The DNA constructs for expressing constructs comprise a 5' requistory region which includes a promoter a construct sequence and adomnstream box element operably linked clament, a leader sequence and adomnstream box element operably linked construct. The DNA constructs of an anamonal reconstruct of the construct. The DNA constructs are used for placed or the construct. The DNA constructs are used to produce the capture of the construct. The DNA construct are used to produce the capture of the construct. The DNA construct are used to produce the capture of the construct of the capture of the construct of the const
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121 ATTTGTTTAACTTTAACAAGAGAATATACATATGCCAACAACAAGACTGGTGGACAGCTA 180
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haemoglobin; enzyme; psbA; T7 phage gene 10; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 182; DB 21; Best Lacal Similarity 100.0%; Pred. No. 1.2e-50; Best Laches 182; Conservative 0; Mismatches 0;
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                                                                             (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ61384 standard; DNA; 1961 BP.
                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 3D; 164pp; English.
              99US-0131611.
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                                                                                                                                     Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Unidentified.
Aequorea victoria.
                                                                                                                                                                                     WPI; 2000-205525/18
              29-APR-1999;
11-JUN-1999;
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                                                                                                                                         Maliga P,
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Gaps

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Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
Prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCAAGCATGACTGGTGGACAGGCTA 180
                                                                                                                                                                                                                                                               1 GAGCTCGCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60
of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
                                                                                                                                                                                                     ;
0
                                                                                     Sequence 5263 BP; 1377 A; 1326 C; 1144 G; 1416 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide seguence of chimeric promoter PrrnLT7g10+DB/pt.
                                                                                                                                                                                                     Indels
                                                                                                                                           100.0%; Score 182; DB 21;
100.0%; Pred. No. 4.3e-50;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "Shine-Dalgarno sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "Prrn plastid promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 3D; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ61374 standard; DNA; 182 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khan MS;
                                                                                                                                                                          Best Local Similarity 100.0%;
Matches 182; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0095167.
98US-0112257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39WO-US17806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0095163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0131611
99US-0138764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .9-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41..144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maliga P, Kuroda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-205525/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200007431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3677 GC 3676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1998;
15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ61374;
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ61374
ប្រព័ន្ធ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a vector of the invention. The specification describes recombinant DNA constructs for expressing heterologous proteins in the plastids of higher plants. The DNA constructs comprise a 5 regularizory region which includes a prometer element, a leader sequence and a downstream box element operably linked to a coding region of the heterologous protein. The chimeric regulatory region enhances translational efficiency of a maNN molecule encoded by the DNA construct. The DNA constructs are used for producing transiscme monocot and dioct plants having high levels of heterologous protein expression. They can be used to drive expression of proteins with aground. Industrial or pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA constructs, for expressing high levels of the reterologous protein in plastical of higher plants, includes promoter, a leader sequence and a downstream box element
                                                                                                                                                                                                                                                                                                                                                                                                   aadA; protein expression; vaccine; haemoglobin; enzyme; psbA;
17 phage gene 10; downstream box; green fluorescent protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c.//tog-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "rice left targeting sequence"
1904..2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/note= "psbA sequence"
                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of plasmid pMSK49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Flg 34A-B; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cocation/Qualifiers
                                                                                                                                                                  AAZ61386 standard; DNA; 5263 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maliga P, Kuroda H, Khan MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0095163.
98US-0095167.
98US-0112257.
99US-0131611.
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                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2103..2823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-205525/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40200007431-A1
                                                                                                                                                                                                                                                                                      19-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1999;
   181 GC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                AA261386;
                                                                                                                                           AAZ61386/c
                                                                                                                RESULT 3
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us-09-762-105a-14.rng

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The present sequence represents a chimeric plastid rRNA operon consequence, to promocer with the PT plage gene and a syntheric downstream for the place gene and a syntheric downstream for the plastids of higher plants. The plastids of higher plants. The DNA constructs for expressing heteroclogues protein as "teglalatory region which includes a promoter constructs comparise a" "teglalatory region which includes a promoter region college and the plastids of higher plants. The DNA constructs comparise a" teglalatory region of the heterologues protein. The chimeric regulatory region enhances translational efficiency of an mixA molecula encoded by the construct. The DNA constructs are used for producing transformed monocot and clot plants baving high levels of heterologues protein agronomic, industrial or plants and to differ expression of proteins with the expression of production for walk meaning production for any meaning production of the mineric meaning production for many meaning miles, sorghum, sugar cane, fice, the heavy of the production of the human man meaning miles, sorghum, sugar cane, fice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tobacco; ribosome binding site; aprotinin; herbicide tolerance; plastid; human growth hormone; insulin; ds.
                                                                                                                                                                               New recombinant DNA constructs, for expressing high levels of thererologous protein in plastids of higher plants, includes promoter, a leader sequence and a downstream box element -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AGGGGCAGGGATGCCTATATTTCTGGGAGGGAGCCACAACGGTTTCCCACTAGAAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGGGGCAGGGATGGCTATATTTCTGGAGGGAGCCACAACGGTTTCCCACTAGAAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGCTCGCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCICGCICCCCCGCCGICGITCAAIGAAAIGGAIAAGAGGCICGIGGGAIIGACGIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCAAGC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ATTTGTTTAACTTTAAGAAGGAGATATACATATGGCTAGC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.6%; Score 159.4; DB 21;
99.4%; Pred. No: 3.6e-43;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161 BP; 43 A; 30 C; 48 G; 40 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prrn/G10L fusion nucleic acid sequence.
                                                                 (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                      Claim 4; Fig 3D; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ88175 standard; DNA; 168 BP
                                                                                                     Khan MS;
           99US-0131611.
99US-0138764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.4%;
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US15472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000 (first entry)
                                                                                                     daliga P, Kuroda H,
                                                                                                                                          PI; 2000-205525/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200003022-A2.
        29-APR-1999;
11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicotiana sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ88175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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           à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a chimeric plastid rRNA operon congarityse (Prem) promoter with the ray plast game and scherichia coli downstream box ribineric promoter 17 plage game and scherichia coli downstream box ribineric promoter 18 used, as a 5' regulatory presents of preduce recombinant but No constructs for expressing hequence. Go preduce recombinant but No constructs for expressing hequence as 1 the plastida of higher plants. The DNA constructs comparise a 5' regulatory region which includes a promoter construct comparise a 5' regulatory region which includes a promoter construct. The DNA construct and to was a coling region of the heterologous protein. The chimeric regulatory the DNA construct are used for producing transformed monocot and dioci plants having high levels of heterologous protein controlled and the plants having high levels of heterologous protein controlled and the plants which can be used to drive expression of proteins with the construct of construct in the name memoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the brane mane will the constructs of the brane mane will be transformed wheat, basiley, oat, type or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; protein expression; vaccine; enzyme; T7 phage gene 10; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AGGGGCAGGGATGCTAATTTCTGGGAGGGAGCCACAACGGTTTCCCACTAGAAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATTTTGTTTAACTTTAAGAAGGAGATATACATATGGCAAGCATGACTGGTGGACAGGCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGCTCGCTCCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAGCTCGCTCCCCCCCCTCGTTCAATGAGAATGGATAAGGAGGCTCGTGGGATTGACGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                          11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of chimeric promoter PrrnLT7g10-DB.
                                                                                                                                                                                                                                                                                                                                                Sequence 182 BP; 47 A; 38 C; 52 G; 45 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- b
/note- "Shine-Dalgarno sequence"
                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
90.3%; Score 164.4; DB 2:
Best Local Similarity 94.0%; Pred. No. 8.3e-45;
Matches 171; Conservative 0; Mismatches 11.
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"Prrn plastid promoter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ61375 standard; DNA; 161 BP.
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98US-0095167.
98US-0112257.
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03-AUG-1998;
15-DEC-1998;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Hajdukiewicz P;
WO200104327-A1.
                                                                                                                                                                                                                                10-JUL-1999;
                                                                         18-JAN-2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF57902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a construct (1) comprising a plant planted to the plant producer region, a DNA sequence capable of conferring herbicide to describe the plant cell and a transcription termination region operably joined in the 5'-3' direction. (1) is useful for producing the best of the plant cell and a plant cell, comprising transforming plantida of the plant cell with (1) and the herbicide tolerance is useful for corression construct is useful for directing expression of DNA sequences encoding enzymes involved in herbicide tolerance or for producing of harmaceutical proteins e.g. human growth hormone, aprothini, insulin or insulin precursors. Transplastomic of plants have high level of tolerance to herbicides. Protein levels obtained from plastid expression constructs in from nuclear expression constructs. Plastid expression constructs utilising 16s thosomal RNA operon (Prin)/G10. promoter/RNS sequence accumulates 50-350 fail higher levels of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    than nuclear expression constructs. By including targeting sequences, the expressed proteins can be targeted to particular suborganellar regions for e.g. thylakoid membrane, which facilitates increased oxidative stability and proper protein folding. Insect or disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 CAGGGATGGCTATATTTCTGGGAGGAGGACCACAACGGTTTCCCACTAGAAATAATTTTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGGATGGCTATATTTCTGGGAGCGA----ACTCCGGGCGAATTGTAGAATAATTTG 138
                                                                                                                                                                                                                                                                                                                                                                                   construct useful for producing herbicide tolerance in plants and directing production of pharmaceutical proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                       Hajduklewicz P, McBride KE, Nehra N, Schaaf DJ, Stalker DM;
Staub JM, Ye G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.2; DB 2
Pred. No. 3.8e-27;
0; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for the production of expression constructs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 6; 62pp; English.
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88.7%;
                               98US-0113257
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                                                                                                        (CALJ ) CALGENE LLC
                                                                                                                                                                                                                                                                                                    WPI; 2000-147617/13
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                               10-JUL-1998;
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Best Local 9
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Nucleotide sequence of Prrn/G10L promoter/RBS hybrid.

AAF25352

ō g ŏ g ő 셤 Plant plastid; herbicide tolerance; EPSPS protein;

G10L ribosome binding site; ds.

Synthetic

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is transcribed in plant cell plastids, and a transcription termination resealon, in the 5'-3 direction of transcription the construct is useful for producing tolerance of a herbicide in a plant cell. The construct is useful also useful for enhancing expression of a died variety of genes, both enkaryotic and prokaryotic, in plant plastids. It is useful for genetic engineering of plant cells and which provide for enhanced expression of EBSPS proteins on their protein in plant cell plastids. The present sequence represents a hybrid comprising plastid 16s Tibosomal RNA operon, and a synthetic Glur Intosome binding site (RBS). The hybrid is used to produce constructs of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes a construct comprising a promoter functional
                                                                                                                                                                                                                                                                         Novel constructs for expressing herbicide tolerance genes in plant cell plastide, comprises a promoter functional in plant plastide, a DNA sequence conferring herbicide tolerance and transcription terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In a plant plastid, a DNA sequence capable of conferring tolerance in a plant cell to at least one herbicide compound when the DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein; GFP; translational fusion; gene expression; herbicide tolerance; pharmaceutical protein; disease resistance; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.2; DB 7
Pred. No. 3.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prrn/G10L promoter/RBS hybrid coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 6; 70pp; English.
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88.7%;
.0-JUL-2000; 2000WO-US18727.
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                                                       99US-0351123
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                                                                                                                                                                                                                     WPI; 2001-138356/14.
                                                                                                              (CALJ ) CALGENE LLC.
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The present sequence represents a chimeric plastid FRNA operon onergo with the present sequences, the type (Frn) promoter with at plastid translation control sequences, or regularizer year effort) promoter with a plastid translation control sequences, without a downstream box. The chimeric promoter is used, as a 5° cregilatory requence, to produce recombinant but a construct so compares a 5° regulatory region within includes a EUR interest of the entertoing protein. The PAR constructs compares a 5° regulatory region within includes a EUR interest of a coding region of the heteologous protein. The Management of the heteologous protein man operation of the heteologous protein man one or and down the construct. The DAN constructs are as of heteologous protein a special of the management of the code of the construct of the construct of the code of th
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prrn promoter; atpB; protein expression; vaccine; enzyme; ss.
                                                                                                                                                                                                                                                                New recombinant DNA constructs, for expressing high levels of thererologous protein in plastical of Higher plants, includes promoter, a leader sequence and a downstream box element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGGGGCCAGGGATGGCTATATTTCTGGGAGGGAGACCACAACGGTTTCCCACTAGAAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AGGGGGCAGGGATGGCTATATTTCTGGGAGAATTAACCGATCGACGTGCAAGCGGACATT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of chimeric promoter PrrnLatpB+DBwt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93.6; DB 21;
Pred. No. 2.8e-21;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 191 BP; 52 A; 32 C; 48 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
"Prrn plastid promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATTTTGTTTAACTTTAAGAAGGAGATATACATATGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TATTTTAAATTCGATAATTTTGCAAAAACATTTCG 156
                                                                                                                       (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
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7..89
                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 3A; 164pp; English.
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                                                                                                                                                                           Khan MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 75.0%;
Matches 117; Conservative
98US-0112257.
99US-0131611.
99US-0131611.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (9-JUN-2000 (first entry)
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                                                                                                                                                                           Kuroda H,
                                                                                                                                                                                                                       WPI; 2000-205525/18.
03-AUG-1998;
15-DEC-1998;
29-APR-1999;
11-JUN-1999;
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                                                                                                                                                                           Maliga P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ61360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X X X E X E X S X X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a construct comprising a promoter region, as DNA sequence encoding at least the first's amino acids of green fluorescent protein (GFP), a DNA sequence encoding a protein of interest and a transcription termination region. Constructs of this type have been shown to enhance gene expression, and they can be used in plants to confer thereforce to the conference, disease resistance and the ability to produce pharmaceutically important proteins on the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
Prrn promoter; atpB; protein expression; vaccine; enzyme; ss.
                                                                                                                                                                                                                           New constructs encoding translational fusion of 14 amino acids derived from green fluoressent protein for enhancing desired protein (5-enclpyruvylahlkimare-3-phosphate synthase) expression in plant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 CAGGGAIGGCIAIAITICTGGGAGGGAGACCACAACGGTTTCCCACTAGAAATAATTTTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 CAGGGATGGCTATATTTCTGGGAGCGA----ACTCCGGGCGAATTGTAGAAATAATTTTG 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 GCTCCCCCCCCGCCGTCGTTCAATGAATGGATAAGAGGCTCGTGGGATTGACGTGAGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of chimeric promoter PrrnLatpB-DB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 168 BP; 45 A; 31 C; 51 G; 41 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114..116
/*tag= b
/note= "Shine-Dalgarno sequence"
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"Prrn plastid promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITAACTITAAGAAGGAGATATACATATGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTAACTTTAAGAAGGAGATATACCCATGG 168
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                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 1; 27pp; English.
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                                     99US-0351124
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Matches 133; Conservative
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                                                                                                                                                                                  WPI; 2001-147195/15.
                                                                                     (CALJ ) CALGENE LLC
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                                 09-JUL-1999;
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                                                                                                                                  Staub JM;
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Gaps

Waliga P,

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mentation between the promoter with atom translation control sequences and mattered downstream box. The chimeric promoter is used, as a 5' sequence, to produce recombinant bNA constructs for expressing heterologous proteins in the plastids of higher plants. The NNA constructs comprise a 5' requiatory region which includes a promoter to accomprise a 5' requiatory region which includes a promoter to a coding region of the heterologous protein. The chimeric requiatory the bNA construct arealstional efficiency of an NNA molecule encoded by the bNA construct. The DNA construct are a new part of a man one of the plants having high levels of heterologous protein expression fleet can be used to trice expression of proteins with agronomic, industrial or pharmacequical importance, including production agronomic.
                                                 Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin; Prrn promoter; atpB; protein expression; vaccine; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA constructs, for expressing high levels of theterologous protein in plastical of higher plants, includes promoter, a leader sequence and a downstream box element -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AGGGGCAGGGATGCCTATATTTCTGGGAGGGAGCCACACGGTTTCCCACTAGAAATA 120
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      Nucleotide sequence of chimeric promoter PrrnLatpB+DBm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
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/note= "Shine-Dalgarno sequence"
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/note= "Prrn plastid promoter"
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0; Mismatches
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                                                                                                                                                               Location/Qualifiers
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75.0%;
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99US-0131611.
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Best Local Similarity 75.0<sup>1</sup>
Matches 117; Conservative
                                                                                                                                                                                                                                                        14..116
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                              X X X X X S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA constructs, for expressing high levels of neterologous protein in plastical of higher plants, includes promoter, a leader sequence and a downstream box element
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0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 227 BP; 58 A; 42 C; 55 G; 72 T; 0 other;
114..116
/*tag= b
/note= "Shine-Dalgarno sequence"
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      misc_signal
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AAZ61362;

AAZ61362 ID AAZ6 XX AC AAZ6 XX DT 19-J

RESULT 11

Query Match

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Green fluorescent protein; GFP; aadA; aptB; protein expression; vaccine; haemoglobin; enzyme; psbA; ss.
                                                                                       Nucleotide sequence of DNA construct FLARE16-S2
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AAZ61382 standard; DNA; 1985 BP.
                                                                                                                                                                   Synthetic.
Unidentified.
Aequorea victoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200007431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-APR-1999;
11-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1998;
15-DEC-1998;
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                           19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-1998
                                AAZ61382;
  DNA fragment designed for CRE-induced expression of recombinant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence was used in an example illustrating an invention relating to a method for mainpulating the genome of higher plants. The method involves selecting plant cells expressing profeins encoded by BNA construct having a nucleic acid encoding a marker, excision sites and plastid tergeting sequence for homologous recombination into a plastid genome at a triget sequence for homologous recombination into a plastid genome at a triget sequence. The method is useful for removing heterologous sequences from the plastid genome, such as selectable marker genes following successful shoilardo of transformed progeny, and for emoving endogenous genes associated with male sterility, clpp tibosomal proteins and ribosomal RNA operon sequences from the plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Removing target nucleic acid sequences e.g. selectable marker genes, genes involved in plant cell metabolism, growth development and fertility from plastid genomes, by Cre-mediated site specific recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%; Score 93.6; DB 22; Length 1049; 75.0%; Pred. No. 5.5e-21; tive. 0; Mismatches 39; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1049 BP; 269 A; 235 C; 282 G; 263 T; 0 other;
                                                                                                                                                                                                     CRE recombinase; plastid genome manipulation; site-specific recombination; ds.
      121 TATTTTAAATTCGATAATTTTTGCAAAAACATTTCG 156
                                                                                                                                                                                                                                                                                                                                                                                                                    (RUTF ) UNIV RUTGERS STATE NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 48; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maliga P, Corneille S, Lutz K;
                                                                                  AAF81268 standard; DNA; 1049 BP
                                                                                                                                                                                                                                                                                                                                                                           21-SEP-1999; 99US-0155007.
                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000WO-US25930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0%;
Matches 117; Conservative.
                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-266071/27
                                                                                                                                                                                                                                                                                    WO200121768-A1.
                                                                                                                                              05-JUN-2001
                                                                                                                                                                                                                                                                                                               29-MAR-2001
                                                                                                                                                                                                                                                        Synthetic.
                                                                                                              AAF81268;
                                                    RESULT 12
AAF81268
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/\*tag- a //tag- a /\*tag- b //stag- b //ocfe- aadA Sequence\* //ocfe- 'green fluorescent protein region'

Location/Qualifiers

(first entry)

/\*tag= d /note= "psbA region"

99WO-US17806 98US-0095167 98US-0112257 99US-0131611 99US-0138764

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The present sequence represents a DNA construct of the invention. The specification describes recombinant box constructs for sepressing heterologous proteins in the plastids of higher plants. The DNA constructs for appressing constructs comprise a 5 regularizatory region which includes a promotic element, a leader sequence and a downstream by claiment operably latory to a coding region of the heterologous protein. When molecules encoded by region enhances translational efficience of the protein construct. The DNA construct. The DNA construct is the DNA construct and dioce plants had been construct and dioce plants had been of the protein of proteins. They can be searched the protein of promotics, head they cannot be reflected to the production of proteins with a groundics, head there are producted like human heamoglobin, industrial or household animae at their expression of proteins with the constructer of the invention include maize, mallet, sorghum, sugar cane, rice, when, builey, out, rye or turf grass.
                                                                                                                                                                                   New recombinant DNA constructs, for expressing high levels of telefologous protein in plateids of higher pants, includes promoter, leader sequence and a downstream box element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1985 BP; 553 A; 431 C; 482 G; 519 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             Misclosure, Fig 30; 164pp; English.
       Khan MS;
Waliga P, Kuroda H,
                                                                                                             WPI; 2000-205525/18.
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Indels 0; Gaps

g ò RESULT 13

1 GAGCTCGCTCCCCCCCCTCCTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60

1 GAGCTCGCTCCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60

ö 셤 ογ Score 93.6; DB 21; Length 1985; Pred. No. 7e-21;

51.4%; 75.0%;

Query Match Best Local Similarity

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The present sequence represents a chimeric plastid rRNA operon moneya-type (Prrn) promoter with psbA translation control sequences, without a downstream box. The chimeric promoter is used, as a 5, requiatory sequence, to produce recombinant DNA constructs for expressing
expression. They can be used to drive expression of proteins with agromomic, industrial or. pharmaceutical importance, including production of vaccines, healthcare products like human haemoglobin, industrial or household enzymes. Plants which can be transformed with the constructs of the invention include maize, millet, sorghum, sugar cane, rice, wheat, barley, oat, rye or turf grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric promoter; plastid rRNA operon omega-type promoter; haemoglobin;
Prrn promoter; psbA; protein expression; vaccine; enzyme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA constructs, for expressing high levels of heterologous proted in phisatids of Higher plants, includes promoter, leader sequence and a downstream box element -
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                   1 GAGCTCGCTCCCCCCCCTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG 60
                                                                                                                                                                                                                                                                                           1 GAGCTCGCCCCCCCCCCCCTCGTTCATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG
                                                                                                                                                                                                                             6
                                                                                                                                                                                      Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of chimeric promoter PrrnLpsbA-DB(+GC).
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                          61 AGGGGCAGGGATGCCTATATTCTGGGAGCAATGCAATAAAGTT 105
                                                                                                                                                                                                                                                                                                                                                     61 AGGGGGCAGGGATGGCTATATTTCTGGGAGGGAGACCACAACGGT 105
                                                                                                                                                                                      DB 21;
                                                                                                                                             Sequence 153 BP; 36 A; 27 C; 47 G; 43 T; 0 other;
                                                                                                                                                                                    Score 92.2; DB 21;
Pred. No. 7.6e-21;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141..144
/*tag= b
/note= "Shine-Dalgarno sequence"
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/note= "Prrn plastid promoter"
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                                                                                                                                                                                    50.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ61372 standard; DNA; 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US17805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0095163
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                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-205525/18.
                                                                                                                                                                                                         Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200007431-A1
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29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter; haemoglobin;
                                                                                                                                                61 AGGGGGCAGGGATGGCTATATTTCTGGGAGAATTAACCGATGGAGGGGACATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant DNA constructs, for expressing high levels of the constructs, for expressing thigher plants, includes promoter, thetecologous protein in plastia of higher plants, includes promoter, leader sequence and a downstream box element
                                                                                                                        61 AGGGGCCAGGGATGGCTATATTTCTGGGAGGGAGCCACAACGGTTTCCCACTAGAAATA 120
  Gaps
                                           GAGCTCGCTCCCCCGCGTCGTTCAATGAGAATGGATAAGAGGCTCGTGGGATTGACGTG
                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric promoter; plastid rRNA operon omega-type promoter; hv
Prrn promoter; psbB; protein expression; vaccine; enzyme; ss.
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequence of chimeric promoter PrintpsbB-DB.
  39;
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/note= "Shine-Dalgarno sequence"
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/note= "Prrn plastid promoter"
138..142
                                                                                                                                                                                                       121 ATTTTGTTTAACTTTAAGAGGAGATATACATATGG 156
                                                                                                                                                                                                                                             121 TATTTTAAATTCGATAATTTTTGCAAAACATTTCG 156
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 3B; 164pp; English.
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98US-0095167.
98US-0112257.
                                                                                                                                                                                                                                                                                                                                               AAZ61369 standard; DNA; 153
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99US-0138764
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
  Conservative
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  117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           AAZ61369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
  Matches
                                                                                                                                                                                                                                                                                                            RESULT 14
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us-09-762-105a-14.rng

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heterologous proteins in the plastids of higher plants. The DNA constructs comprises a regular and constructs comprises a regular and constructs comprises and a frequency region which includes a promoter element a leader sequence and a downstream box element operably linked a construct are according region of the heterologous protein. The chimetic regulatory region of the heterologous protein construct. The DNA construct and ensemble consider the DNA construct and ensemble the sequence of proteins of proteins of expression of proteins of proteins of proteins of proteins of proteins of proteins of way construct and short plant having high levels of heterologous protein agroement, including production of vaccines, healthcare products like human beamed subthing production household enzymes. Diants which can be transformed which the construct household enzymes. They or turf grass a miller, sorghum, sugar cane, rice,
         8.566666666666568688
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ö Gaps ó Ouery Match 50.7%; Score 92.2; DB 21; Length 185; Best Local Similarity 88.5%; Pred No. 8.2e-21; Indels 0; Matches 100; Conservative 0; Mismatches 13; Indels 0; Q å

Sequence 185 BP; 47 A; 35 C; 51 G; 52 T; 0 other;

. 61 AGGGGCAGGGATGCTATATTCTGGAACAAAAGCCTTCCATTTCTATT 113 ò

Search completed: May 25, 2003, 13:45:18 Job time : 213 secs